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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=10; day=21; hr=10; min=55; sec=1; ms=429;]

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Application No: 10559986 Version No: 3.0

Input Set:**Output Set:**

Started: 2009-10-05 16:44:05.420
Finished: 2009-10-05 16:44:10.734
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 314 ms
Total Warnings: 46
Total Errors: 0
No. of SeqIDs Defined: 100
Actual SeqID Count: 100

Error code	Error Description
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Input Set:

Output Set:

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Error code	Error Description
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SEQUENCE LISTING

<110> Nestec S.A.; Cornell Research Foundation, Inc.

<120> Modulation Of Coffee Flavour Precursor Levels In Green Coffee Grains

<130> PAT 60100W-1

<140> 10559986

<141> 2006-09-11

<150> EP 03394056.0

<151> 2003-06-20

<160> 100

<170> PatentIn version 3.5

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Met Met Met Thr Ser Gly Gly Leu Met Leu Thr Cys Thr Leu Ala Ile

1 5 10 15

acc ctc tta tcc tgc gca ctc atc tct tca acc act ttc caa cat gaa 217

Thr Leu Leu Ser Cys Ala Leu Ile Ser Ser Thr Thr Phe Gln His Glu

20 25 30

att cag tat cga gta caa gac ccg tta atg ata cgc caa gtc acc gac 265

Ile Gln Tyr Arg Val Gln Asp Pro Leu Met Ile Arg Gln Val Thr Asp

35 40 45

aat cac cac cac cgc cac cac cca ggt agg tct tct gca aac cat cgt 313

Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg

50 55 60

cta	ctg	ggc	acc	acc	aca	gag	ggt	cac	ttc	aag	tcc	ttc	gtg	gag	gag	361
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tac	gag	aaa	act	tac	tct	acg	cac	gag	gag	tac	gtg	cac	cgc	ctg	ggg	409
Tyr	Glu	Lys	Thr	Tyr	Ser	Thr	His	Glu	Glu	Tyr	Val	His	Arg	Leu	Gly	
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Pro	Ser	Ala	Ile	His	Gly	Val	Thr	Gln	Phe	Ser	Asp	Leu	Thr	Glu	Glu	
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Glu	Phe	Glu	Ala	Thr	Tyr	Met	Gly	Leu	Lys	Gly	Gly	Ala	Gly	Val	Gly	
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gtg	atg	atg	gat	gta	tct	gat	ttg	ccg	gag	agt	ttt	gat	tgg	aga	gaa	649
Val	Met	Met	Asp	Val	Ser	Asp	Leu	Pro	Glu	Ser	Phe	Asp	Trp	Arg	Glu	
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Trp	Ala	Phe	Ser	Thr	Thr	Gly	Ala	Ile	Glu	Gly	Ala	Asn	Phe	Ile	Ala	
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act	ggc	aag	ctt	ctc	agc	cta	agt	gaa	cag	cag	ctt	gtg	gat	tgt	gat	793
Thr	Gly	Lys	Leu	Leu	Ser	Leu	Ser	Glu	Gln	Gln	Leu	Val	Asp	Cys	Asp	
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His	Met	Cys	Asp	Leu	Lys	Glu	Lys	Asp	Asp	Cys	Asp	Asp	Gly	Cys	Ser	
225					230					235					240	
gga	ggg	cta	atg	aca	act	gct	ttc	aac	tac	ttg	ata	gag	gca	gga	ggg	889
Gly	Gly	Leu	Met	Thr	Thr	Ala	Phe	Asn	Tyr	Leu	Ile	Glu	Ala	Gly	Gly	
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Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly	
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ggg gtg tca tgt cct ctt att tgt gac aaa aag agg atc aac cat ggt	1129
Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly	
325 330 335	
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Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu	
340 345 350	
ggc tac aag cca tac tgg att atc aag aac tca tgg ggg aag cgt tgg	1225
Gly Tyr Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Lys Arg Trp	
355 360 365	
ggc gaa cat ggt tgc tac cgg ctt tgt cga ggg cac aac atg tgt gga	1273
Gly Glu His Gly Cys Tyr Arg Leu Cys Arg Gly His Asn Met Cys Gly	
370 375 380	
atg agc aca atg gtt tca gct gtg gtg aca cag acc tct tga	1315
Met Ser Thr Met Val Ser Ala Val Val Thr Gln Thr Ser	
385 390 395	
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tatcatgttt tcgaaatatt taggtttgta taatatgaag ggtagagagt aataagaacc	1435
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Asn His His His Arg His His Pro Gly Arg Ser Ser Ala Asn His Arg	
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Tyr Glu Lys Thr Tyr Ser Thr His Glu Glu Tyr Val His Arg Leu Gly
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Ile Phe Ala Lys Asn Leu Ile Lys Ala Ala Glu His Gln Ala Met Asp
100 105 110

Pro Ser Ala Ile His Gly Val Thr Gln Phe Ser Asp Leu Thr Glu Glu
115 120 125

Glu Phe Glu Ala Thr Tyr Met Gly Leu Lys Gly Gly Ala Gly Val Gly
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Gly Thr Thr Gln Leu Gly Lys Asp Asp Gly Asp Glu Ser Ala Ala Glu
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Val Met Met Asp Val Ser Asp Leu Pro Glu Ser Phe Asp Trp Arg Glu
165 170 175

Lys Gly Ala Val Thr Glu Val Lys Thr Gln Gly Arg Cys Gly Ser Cys
180 185 190

Trp Ala Phe Ser Thr Thr Gly Ala Ile Glu Gly Ala Asn Phe Ile Ala
195 200 205

Thr Gly Lys Leu Leu Ser Leu Ser Glu Gln Gln Leu Val Asp Cys Asp
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His Met Cys Asp Leu Lys Glu Lys Asp Asp Cys Asp Asp Gly Cys Ser
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Gly Gly Leu Met Thr Thr Ala Phe Asn Tyr Leu Ile Glu Ala Gly Gly
245 250 255

Ile Glu Glu Glu Val Thr Tyr Pro Tyr Thr Gly Lys Arg Gly Glu Cys
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Lys Phe Asn Pro Glu Lys Val Ala Val Lys Val Arg Asn Phe Ala Lys
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Pro Leu Ala Ile Gly Leu Asn Ala Val Phe Met Gln Thr Tyr Ile Gly
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Gly Val Ser Cys Pro Leu Ile Cys Asp Lys Lys Arg Ile Asn His Gly
325 330 335

Val Leu Leu Val Gly Tyr Gly Ser Arg Gly Phe Ser Ile Leu Arg Leu
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Met Ala Lys Pro Ser Ser Ser Leu Leu Thr Leu
1 5 10

cct tcc ttt ctt ctg atc ttt ttc att ctt gca cta ttt tcc acc acc 159
Pro Ser Phe Leu Leu Ile Phe Phe Ile Leu Ala Leu Phe Ser Thr Thr
15 20 25

ctc caa gtt aat gcc ttg gga agg aaa gtg gga gca agg gag aag att 207
Leu Gln Val Asn Ala Leu Gly Arg Lys Val Gly Ala Arg Glu Lys Ile
30 35 40

gag gat gtg aag agc aac aaa gaa gtt caa gaa ctt ggg gaa tat tgt 255
 Glu Asp Val Lys Ser Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys
 45 50 55

gtt tct gag tac aac aag agt ttg cgg aag aag aac aac gaa agt ggt 303
 Val Ser Glu Tyr Asn Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly
 60 65 70 75

gct cct ata atc ttc aca tct gtg gtg gag gct gag aag cag gtg gtt 351
 Ala Pro Ile Ile Phe Thr Ser Val Val Glu Ala Glu Lys Gln Val Val
 80 85 90

gct ggg atc aaa tat tat ctc aag att aag gcc acc act tct tct ggg 399
 Ala Gly Ile Lys Tyr Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly
 95 100 105

gtt ccc aag gtt tac gat gcc att gtg gtg gtt cgg cct tgg gtt cat 447
 Val Pro Lys Val Tyr Asp Ala Ile Val Val Val Arg Pro Trp Val His
 110 115 120

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 Thr Lys Pro Arg Gln Leu Leu Asn Phe Ser Pro Ser Pro Ala Thr Lys
 125 130 135

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attattagta cctttcagtg caaattctct ttgctgttaa gtgttcgggtt tttttttttt 608

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Asn Lys Glu Val Gln Glu Leu Gly Glu Tyr Cys Val Ser Glu Tyr Asn
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Lys Ser Leu Arg Lys Lys Asn Asn Glu Ser Gly Ala Pro Ile Ile Phe
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Thr Ser Val Val Glu Ala Glu Lys Gln Val Val Ala Gly Ile Lys Tyr
85 90 95

Tyr Leu Lys Ile Lys Ala Thr Thr Ser Ser Gly Val Pro Lys Val Tyr
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aaaaatccat tcttgggaatt catttatcca tatacacccat acttgtgcat gtcccttttg 180
gttggttttg ttttgatgata agtaattggt ggtttattgg tttttcatga tggctccgga 240
tctaagaaga aatgggtcgg tagtagcttt agccctgtta gtctctctgg ttgttaatgg 300
tggtattttt gatgtagaag gtaacaataa tgtgggtttt gaggtggaac ataaatttaa 360
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tcccaccgcc atggcaga atg ctt gca gcc ctt gac atg cct ttg ggt ggc 471
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Asn Gly Ser Pro Thr Asp Ala Ala Leu Tyr Phe Thr Lys Leu Ser Ile

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Ile Leu Trp Val Asn Cys Ala Gly Cys Val Arg Cys Pro Lys Lys Ser			
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Ser Leu Gly Ile Asp Leu Thr Leu Tyr Asp Met Lys Ala Ser Ser Thr			
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Gly Arg Leu Val Thr Cys Asp Gln Asp Phe Cys Leu Ser Ala Phe Asn			
80	85	90	
gcc cca gcc tct gat tgc aag gtt ggt aac ccc tgt gca tat tct gtt			759
Ala Pro Ala Ser Asp Cys Lys Val Gly Asn Pro Cys Ala Tyr Ser Val			
95	100	105	
act tac gga gac ggg agc tca acc ggc gga tat ttt gtc aga gac tat			807
Thr Tyr Gly Asp Gly Ser Ser Thr Gly Gly Tyr Phe Val Arg Asp Tyr			
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Ala Lys Leu Asn Gln Leu Thr Gly Asn Leu Gln Thr Ile Pro Met Asn			
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Ser Ser Ile Ile Ser Gln Leu Ala Ser Ala Gly Lys Val Lys Lys Ile			
175	180	185	
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Phe Ser His Cys Leu Asp Gly Ile Asn Gly Gly Gly Ile Phe Ala Ile			
190	195		